REMARKS/ARGUMENTS

Re-examination and favorable reconsideration in light of the following comments are respectfully requested.

Claims 1 - 48 are pending in the application. Currently, no claim stands allowed.

In the office action mailed November 13, 2003, claims 1 - 41 were rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. Additionally, claims 1 - 5, 34, and 41 were rejected under 35 U.S.C. 102(b) as being anticipated by the Michalewicz article.

The foregoing rejections are traversed by the instant response.

The rejection under 35 U.S.C. 112, first paragraph, is in error because the specification in the instant specification goes into great detail to explain how each of the claimed method steps is performed. Thus, one of ordinary skill in the art having the instant specification before him/her could easily perform the method of the present invention and could form the system of the claimed invention. While the details involving how one steps from the chromosomes to a fully descriptive model may not be identified in a manner accustomed to by the Examiner, they are in the specification and would be well understood by any person skilled in the art.

Beginning on page 12 of the specification, there is a disclosure of how the method of the present invention converts a binary chromosome into a predictive model. As indicated thereon, each chromosome consists of a plurality of observed variable segments, each formed by a plurality of genes, and a plurality of interaction segments, each formed by a plurality of genes. The genes that comprise each observed variable segment (for a continuous variable) are as follows: (1) include/exclude

(or selection) gene; (2) minimum and maximum Outlier gene; (3) transformation gene; and (4) coefficient gene. See page 13, lines 11 et seq. As set out on page 14, et seq., the include/exclude gene is encoded as a "1" for a variable that is included, and a "0" for a variable that is excluded. One of ordinary skill in the art with this information will understand that the portion of the predictive model that is generated by the include/exclude gene is simply Boolean selection logic.

The Outlier gene is encoded as two binary strings representing positive numbers, one for minimum Outlier value, and one for maximum. The number of bits used for each Outlier value is programmable. If for example 4 Outlier bits are used, the Outlier bit string will range from 0 to 15, where 15 represents 15/15 or 100% of the range. On page 17, line 3, et seq., and FIG. 3 describe how the range between the median and the maximum, and between the median and the minimum, would be divided up by a 4-bit Outlier Gene. The 4-bit number is converted to its component of the predictive model.

The transformation gene, as described on page 21, et seq., allows for power transformation to be applied. Some number of bits represents the exponent to use in the power transformation. As stated in this section of the specification, the desired precision (number of bits) and desired range determine how the exponents are represented. For example, with a range of 4 (power of -2 to 2), and a precision of 3 bits, the following table shows all possible transformations:

bits	Exponent	Transformation
000	4 * 0/8 - 2	x ** -2
001	4 * 1/8 - 2	x ** -1.5
010	4 * 2/8 - 2	x ** -1.0
011	4 * 3/8 - 2	x ** -0.5
100	4 * 4/8 - 2	log(x)
101	4 * 5/8 - 2	x ** 0.5
110	4 * 6/8 - 2	x ** 1.0 (=x)
111	4 * 7/8 - 2	x ** 1.5

The coefficient gene provides a coefficient to be multiplied by the input data value, once Outlier trimming and any transformation has been performed. There are many well known methods for representing floating point numeric values as a "plurality of bits". For example, one having the instant specification before him/her, would understand that the coefficient genes can be encoded as a 2's complement integer, divided by the maximum (absolute) value that can be represented, to yield a value between -1.0 and 1.0. So for an 8 bit coefficient, the minimum value is 1000000 (-128 integer, for a coefficient of -128/128 = -1.0). The maximum value is 01111111 (127 integer, for a coefficient of 127/127 = 1.0).

The following example illustrates how an entire chromosome can be converted from a binary string to a predictive model.

Given 3 variables called VAR1, VAR2 and VAR3, all with a range of 0.0-1.0 with a median value of 0.5.

For this example, 4-bits will be used for each outlier (min and max), 3 bits for a transformation, and 8 bits for a coefficient. Along with the 1-bit include/exclude gene, this totals 15 bits per variable.

VAR1: 0 0011 0100 011 11011001

VAR2: 1 0101 0010 010 00010111

VAR3: 1 1000 0011 110 00111000

The following binary string would represent the entire chromosome:

000110100011110110011010100100100001011111000001111000111000

To convert the binary string to an equation, first select variables with the include/exclude gene bit set (VAR2 and VAR3).

Perform outlier trimming for VAR2 as follows:

VAR2 minimum trim percentage = 0101/1111 = 5/15 = 33.33%

VAR2 minimum value = min + 0.3333 * (median - min)
= 0 + 0.3333 * (0.5 - 0.0)
= 0.1667

VAR2 maximum trim percentage = 0010/1111 = 2/15 = 13.33%

VAR2 maximum value = max - 0.1333 * (max - median)
= 1.0 - 0.1333 * (1.0 - 0.5)
= 0.9333

Next VAR2 must be transformed, using transformation 010 (VAR2 to the power -1, or 1/VAR2).

Then VAR2 is multiplied by the coefficient value:

00010111 (23 decimal)

23/127 = 0.18

Perform Outlier trimming for VAR3:

VAR3 minimum trim percentage = 1000/1111 = 8/15 = 53.33%

VAR3 minimum value = min + 0.5333 * (median - min)
= 0 + 0.5333 * (0.5 - 0.0)
= 0.2667

VAR3 maximum trim percentage = 011/1111 = 3/15 = 20%

VAR3 maximum value = max - 0.20 * (max - median)
= 1.0 - 0.20 * (1.0 - 0.5)
= 0.9

No transformation is selected for VAR3 (since the Transformation Gene is 110, yielding an exponent of 1), so the

trimmed value just needs to be multiplied by the coefficient value:

00111000 (56 decimal)

56/127 = 0.44

The entire final predictive model is represented by the following pseudo-code:

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SCORE = 0.0
IF (VAR2 < 0.1667) VAR2 = 0.1667
IF (VAR2 > 0.9333) VAR2 = 0.9333
SCORE = SCORE + (0.18 * (1 / VAR2))

IF (VAR3 < 0.2667) VAR3 = 0.2667
IF (VAR3 > 0.9) VAR3 = 0.9
SCORE = SCORE + (0.44 * VAR3)
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The preceding does not describe the interaction terms, which follow the pre-variable gene segments. As specified on page 12 of the specification, each chromosome consists of a plurality of observed variable segments, followed by a plurality of interaction segments. As described in the portion beginning on page 23, line 8 and extending to page 26, line 2, each interaction segment consists of an Include/Exclude (or selection) portion, two variable indices, one operation index, and a coefficient value. As set out on page 24, line 14 et seq., the operator index simply represents a selection from the following set of operations:

bits	Interaction
000	VAR1 + VAR2
001	VAR1 * VAR2
010	VAR1 / VAR2
011	VAR1 - VAR2
100	$(VAR1 - VAR2)^2$
101	$\lvert VAR1 - VAR2 \rvert$

The first and second variable genes describe the variable selection portion of the interaction term. Assuming 4 bits for variable selection (which is limited to 15 total variables on the chromosome) and an 8-bit coefficient, an interaction gene could look like:

I/E	1st	2nd	Op	Coefficient
1	0011	0101	001	01000001

011 (3 decimal) refers to the 3rd observed variable, and 0101 refers to variable number 5. The binary code 001 represents the multiplication operation, and the coefficient 01000001 represents: (65 decimal)

65/127 = 0.51

The sample Interaction Gene would be converted to a predictive model as follows:

0.51 * (VAR3 * VAR5)

As can be seen from the foregoing discussion, the specification in the instant application fully describes how a chromosome comprises a fully predictive model. Certainly, each of the steps set out in method claims 1 - 33 and each limitation in system claims 34 - 41 are fully and completely described in the specification. Section 112 of the patent statute requires nothing more. The Examiner is hereby requested to withdraw the rejection under 35 U.S.C. 112, first paragraph.

With regard to the anticipation rejection of claims 1 - 5, 34, and 41 over the Michalewicz, while the cited reference uses a genetic algorithm to generate an equation to solve for a dependent variable based on the values of at least one independent variable, it does not anticipate using a genetic algorithm to generate a predictive model. A predictive model, while it can take the form of an equation, is more complex then the mathematical equation that Michalewicz hopes to create. In

the creation of a predictive model, the selection of which independent variables to use is as important as determining the value of the coefficients in the equation. In the instant application, a genetic algorithm is used to determine which variables from a data set should be used. Additionally, the transformation and manipulations that can be applied to an independent variable such as Outlier trimming and variable transformation are part of a predictive model. Further, creating interaction terms between independent variables that could be used in the predictive mode in addition to using independent variables by themselves is needed. All of these features, variable selection and data preparation are parts of the predicative model that is created by the present invention. They are not however part of the equation Michalewicz generates.

With regard to claim 1, it is allowable because Michalewicz does not perform each of the steps set out therein. In particular, Michalewicz does not perform the step of creating from said database of an initial generation of chromosomes each comprises a predictive model.

With regard to claims 2 and 3, these claims are allowable for the same reason as claim 1, as well as on their own accord. Michalewicz does not determine the new fitness measures and repeats steps (e) and (f) in combination with the other claimed steps.

With regard to claim 4, the random method for creating an initial generation for chromosomes that is implemented by the present invention is different from the Michalewicz method. In the present invention, values are randomly assigned to genes within each observed variable segment. Michalewicz does not anticipate randomly assigning values of Boolean type such as used in the present invention in an include/exclude gene or the

other types of values assigned to other genes such as Outlier, contrast, transformation, and interaction genes. It is submitted that Michalewicz does not teach or suggest the initial generation chromosome creating step of the present invention.

With regard to claim 5, the distributed method for creating an initial generation for chromosomes is not random and differs from what is described in the Michalewicz method. As described in the specification, a process is used by which the initial population is generated. Because a clearly defined process is used to generate the distributed population, it is not random and thus, the process differs from Micahelwicz's. The instant process creates two chromosomes for each observed variable where only one independent variable is used in the predictive model. The first of the two chromosomes has a positive coefficient for the only variable in the model while the second has a negative coefficient. Michalewicz's distributed process selects points from the boundary of the solution space, and will use every variable in the equation.

Claim 34 is a system claim which corresponds to claim 1. It is allowable for the same reasons that claim 1 is allowable. Michalewicz does not teach or suggest the system elements set forth in claim 34.

With regard to claim 41, Michalewicz does not anticipate using a chromosome to represent an equation for numerical optimization problem and for representing a predictive model. A predictive model contains a plurality of observed variable segments each of which contains several genes. One of the genes which is included in a variable segment is an include/exclude gene which determines if this variable should be included in the predictive model. Michalewicz does not allow the genetic algorithm to determine which variables are used in his equation

nor having the chromosome include a representation of this decision. Other genes that may be included are Outlier trimming and transformation genes which modify the data being input into the predictive model. Michalewicz does not allow the genetic algorithm to alter the data being input into his equation nor having the chromosome include a representation of these alterations. Michalewicz does not allow both continuous (numerical) and categorical (character) data to be input into his equation, but only allows numeral data to be input into the equations. A plurality of interaction segments is also included in a predictive model. An interactive segment is used if two observed variables have predicative value when used together and does not simply represent the substitution of a variable with an independent equation such as that used by Michalewicz. The elements set forth in claim 41 can not be found in Michalewicz. Thus, claim 41 is allowable for the same reasons as claim 34, as well as on its own accord.

For the foregoing reasons, the claims in the application are believed to be allowable. Such allowance is respectfully solicited.

Should the Examiner believe an additional amendment is need to place the case in condition for allowance, he is hereby invited to contact Applicants' attorney at the telephone number listed below.

A three month extension of time is enclosed herewith along with a check in the amount of $475.00 to cover the extension of time fee. Should the Commissioner determine that an additional

fee is due, he is hereby authorized to charge said fee to Deposit Account No. 02-0184.

Respectfully submitted,

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I, Nicole Motzer, hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: "Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313" on May 13, 2004.

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